Supporting Information

Dinuclear copper(II) complexes of a polybenzimidazole ligand: their structures and induction roles in DNA condensation

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Experimental section

All chemicals were of reagent grade as received from commercial sources and used without further purification.

The ligand dtpb was prepared according to the earlier reported method.¹ And the ligand Bis(benzimidazol-2-yl-methyl)amine (IDB) was prepared according to the method described by Adams et al.²

Preparation of **1**. A clear blue methanol solution (20 mL) containing 0.2 mmol dtpb and 0.4 mmol CuCl₂·2H₂O after stirring for 2 h was obtained and left at room temperature without disturbing. Slow evaporation of solvents gave blue plate crystals of **2** (yield: 30%). Elemental analysis (%), calcd for $C_{46}H_{59}O_6N_{13}Cl_4Cu_2$: C47.64, H5.09, N15.70; found: C49.52, H4.70, N 16.65. IR data (cm⁻¹): 3390, 3055, 1621, 1593, 1452, 1275, 1078, 853, and 748.

Preparation of **2**. Crystals of **2** (0.05 mmol) and Cu(NO₃)₂·3H₂O (0.1 mmol) were dissolved in methanol (10 mL) and stirred for 30 min. The resulting clear blue solution was left at room temperature without disturbing. Slow evaporation of solvents gave blue plate crystals of **3** (yield: 40%). Elemental analysis (%), calcd for $C_{46}H_{55}Cl_2Cu_2N_{15}O_{10}$: C46.94, H4.77, N17.86; found: C47.50, H4.28, N18.85. IR data (cm⁻¹): 3066, 1623, 1553, 1390, 1363, 1286, 1052, 823, and 748.

Preparation of $[Cu(idb)Cl_2]CH_3OH$. This complex was synthesized by reaction of IDB (0.2mmol) and 0.2 mmol CuCl₂·2H₂O in 30ml methanol solution at 333 K for 2 h. The resulting solution was filtered and blue block crystals

suitable for X-ray diffraction were obtained by slow evaporation of the filtrate at room temperature overnight (yield: 30%). Elemental analysis (%), calcd for C₁₇H₁₉Cl₂CuN₅O: C 46.01, H 4.31, N 15.78; found: C45.98, H4.43, N15.72. IR data (cm⁻¹): 3364, 3065, 1659, 1573, 1400, 1109, 727 and 627.

Physical measurments

C, H, N elemental analysis was performed on a Vario EL III elemental analyzer. The infrared spectrum was recorded on KBr pellets with a NEXUS470–IR spectrometer in the range of 400–4000 cm⁻¹.

All the data were collected on a Nonius Kappa CCD diffractometer with Mo *Ka* radiation ($\lambda = 0.71073$ Å). Empirical absorption corrections were applied using the multi-scan program. The structures were solved by direct (or patterson) methods and refined by full-matrix least-squares on F^2 with anisotropic thermal parameters for all non-hydrogen atoms with the SHELX-97 program.^{3,4} For compounds 1-3, all of the non-hydrogen atoms (except for some solvent molecules in some cases) were refined with anisotropic thermal motion parameters, and the contribution of the hydrogen atoms was included in calculated positions.

For dtpb, O1w was located at the special position of the inversion center and O5w was refined with its occupancy constrained to be 0.5. Owing to the serious crystal deterioration, although the crystals selected were sealed in capillaries with mother liquid, some of the non-coordinated solvent molecules could not be modeled by discrete atoms in **1** and **2**. The contribution of the solvent to the diffraction pattern was subtracted using the SQUEEZE procedure of PLATON (Spek, 2003).⁵

For 1, five water and two methanol molecules have been determined during the structural refinement. The contributions of the rest solvent molecules are subtracted using SQUEEZE procedure. The voids are 901.1 Å³ per unit cell (consisted of about 8.17% percent of the crystal volume, equally distributed across four cavities), corresponding to additional 5~6 H₂O molecules. A similar treatment was performed in refinement of **2**. The voids (626 Å³) were found and additional 7~8 water molecules should be included in each coordination compound molecule. In both 1 and 2, the hydrogen atoms bonded to solvent molecules are not fully positioned. Owing to the serious disorder of the solvent molecules, some short intermolecular contacts have been caused in the CheckCIF report. These contacts should be omitted.

For $[Cu(idb)Cl_2]CH_3OH$, the aimine N atom was disordered over two positions. The final occupancies for the major and minor components are 0.54(1) and 0.46(1), respectively. H atoms bonded to C atoms were located at the geometrical positions and H atoms bonded to N and O atoms were found from the difference maps with the constraints of N-H=0.86(1)Å and O-H=0.82(1)Å.

Table S1. Crystal parameters of dtpb and mono- and dinuclear Cu(II) complexes

	1	2	dtpb	[Cu(idb)Cl ₂]CH ₃ OH	
empirical formula	$(C_{44}H_{43}Cl_2Cu_2N_1$ 3)·(H ₂ O) ₄ ·(CH ₃ O	$(C_{44}H_{45}Cl_2Cu_2 N_{13}O) \cdot (CH_3OH)$	$(C_{44}H_{43}N_{13})\cdot(H_2O)_{3.5}$	$(C_{16}H_{15}Cl_2CuN_5) \cdot (C H_3OH)$	
F 1 11/	$H)_2 \cdot Cl_2$	$)_{2} \cdot (NO3)_{2} \cdot H_{2}O$	005.07	142.01	
Formula weight	1158.85	1176.01	825.97	443.81	
Crystal system	Monoclinic	Triclinic	Orthorhombic	Orthorhombic	
Space group Unit cell	C2/c	<i>P</i> -1	C222 ₁	Pbca	
dimensions					
a (Å)	28.1248(16)	13.6420(6)	8.3956(5)	14.0278(3)	
b (Å)	20.2139(10)	15.0146(6)	29.5409(18)	14.3718(3)	
c (Å)	19.4855(10)	16.3045(7)	35.872(2)	18.2724(5)	
α (°)	90	70.145(1)	90	90	
β (°)	95.672(1)	86.293(1)	90	90	
γ (°)	90	81.483(1)	90	90	
Volume ($Å^3$)	11023.5(10)	3106.1(4)	8896.8(9)	3683.80(15)	
Z	8	2	8	8	
Calculated density (Mg/m ³)	1.383	1.255	1.232	1.600	
F(000)	4712	1212	3496	1816	
Crystal size	0.20×0.1 0×0.06	0.20×0.10×0.10	0.30×0.20×0.20	0.23 ×0.16 × 0.10	
θ range (°)	1.58-25.00	1.95-25.00	1.49-25.00	2.23-28.28	
Reflections collected	48636	29442	25509	40793	
Independent reflections	9675	10724	4328	4492	
Number of parameters	613	692	555	261	
Goof %	1.082	0.916	0.891	0.980	
Final R indices	R ₁ =0.0716	R ₁ =0.0782	$R_1 = 0.0581$	R ₁ =0.0463	
[I>2σ(I)]	WR ₂ =0.1772	WR ₂ =0.2172	WR ₂ =0.1302	WR ₂ =0.1215	
R indices (all	R ₁ =0.1503	R ₁ =0.1136	R ₁ =0.099	R ₁ =0.0724	
data)	WR ₂ =0.2029	WR ₂ =0.2374	$WR_2 = 0.1418$	WR ₂ =0.1286	
Largest diff. peak and hole(eÅ ⁻³)	0.878, -0.596	0.963, -0.475	0.337, -0.300	0.942, -0.733	

Table S2. Selected bond lengths (Å) and angles (°) data for 1, 2 and $[Cu(idb)Cl_2]CH_3OH$.

1		2		[Cu(idb)C	[Cu(idb)Cl ₂]CH ₃ OH	
Bond distances				·		
Cu1-N2	2.515(5)	Cu1-N1	2.506(3)	Cu1-N1	2.031(8)	
Cu1-N1	2.130(5)	Cu1-N3	2.124(4)	Cu1-N2	1.985(3)	
Cu1-N6	1.966(5)	Cu1-N11	1.965(5)	Cu1-N4	1.990(4)	
Cu1-N4	1.973(6)	Cu1-N13	1.956(4)	Cu1-Cl1	2.602(2)	
Cu1-Cl1	2.241(2)	Cu1-Cl1	2.239(1)	Cu1-Cl2	2.267(1)	
Cu2-N8	1.982(5)	Cu2-N2	2.200(4)			
Cu2-N10	2.145(5)	Cu2-N7	1.950(4)			
Cu2-N12	1.990(5)	Cu2-N9	1.931(4)			
Cu2-N3	2.300(4)	Cu2-Cl2	2.329(2)			
Cu2-Cl2	2.278(2)	Cu2-O1	2.390(4)			
Bond angles				·		
N1-Cu1-N2	80.88(14)	N1-Cu1-N3	81.72(14)	N1-Cu1-N2	80.0(3)	
N2-Cu1-N6	88.03(18)	N1-Cu1-N11	93.12(14)	N1-Cu1-N4	79.2(3)	
N2-Cu1-N4	101.29(14)	N1-Cu1-N13	100.71(14)	N1-Cu1-Cl1	103.6(7)	
N2-Cu1-Cl1	104.58(14)	N1-Cu1-Cl1	99.00(12)	N1-Cu1-Cl2	156.0(7)	
N1-Cu1-N6	81.9(2)	N3-Cu1-N11	82.99(19)	N2-Cu1-N4	158.83(16)	
N1-Cu1-N4	80.8(2)	N3-Cu1-N13	81.09(17)	N2-Cu1-Cl1	93.97(12)	
N1-Cu1-Cl1	174.54(14)	N3-Cu1-Cl1	178.83(13)	N2-Cu1-Cl2	98.94(11)	
N4-Cu1-N6	158.8(2)	N11-Cu1-N13	157.11(11)	N4-Cu1-Cl1	94.95(12)	
N6-Cu1-Cl1	97.96(16)	N11-Cu1-Cl1	97.88(15)	N4-Cu1-Cl2	98.28(11)	
N4-Cu1-Cl1	98.02(17)	N13-Cu1-Cl1	97.86(12)	Cl1-Cu1-Cl2	100.40(6)	
N3-Cu2-N8	78.42(18)	N2-Cu2-N7	79.79(17)			
N3-Cu2-N10	75.89(17)	N2-Cu2-N9	81.98(18)			
N3-Cu2-N12	93.56(18)	N2-Cu2-O1	118.68(16)			
N3-Cu2-Cl2	172.11(13)	N2-Cu2-Cl2	151.40(14)			
N8-Cu2-N10	114.4(2)	N7-Cu2-N9	158.8(2)			
N8-Cu2-N12	142.7(2)	N7-Cu2-O1	100.8(2)			
N8-Cu2-Cl2	96.02(14)	N7-Cu2-Cl2	94.95(14)			
N10-Cu2-N12	98.30(19)	N9-Cu2-O1	96.25(17)			
N10-Cu2-Cl2	101.73(14)	N9-Cu2-Cl2	97.66(15)			
N12-Cu2-Cl2	94.24(14)	O1-Cu2-Cl2	89.90(13)			

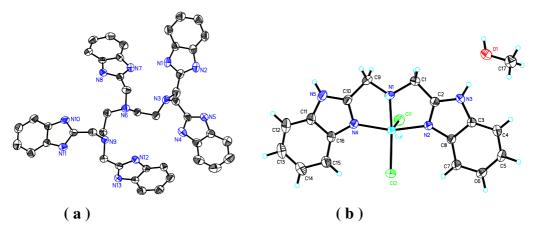
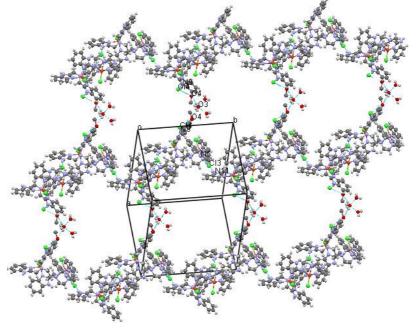
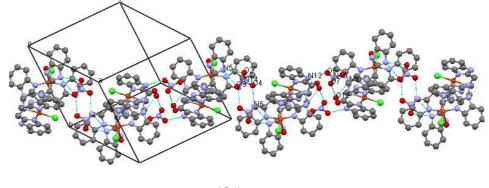


Figure S1. ORTEP view of the ligand dtpb (\mathbf{a}) and [Cu(idb)Cl₂]CH₃OH (\mathbf{b}). For clarity, solvent molecules and hydrogen atoms are omitted.



(**a**)



(**b**)

Figure S2. (a) Showing the formation of the 2-D hydrogen bond network in 1 by the combinative actions of N9...Cl4...O4...O3...O4...Cl4...N9A and N5...Cl3...N11 hydrogen bonded linkages, some solvent molecules not involved in the motif have been omitted for clarity;

(b) Showing the formation of the one-dimensional chains in 2 by the combinative actions of N5...O2/O3-N14-O4...N6 and N8...O12...O7-N15-O6...N12 hydrogen bonded linkages, some solvent molecules not involved in the motif have been omitted for clarity.

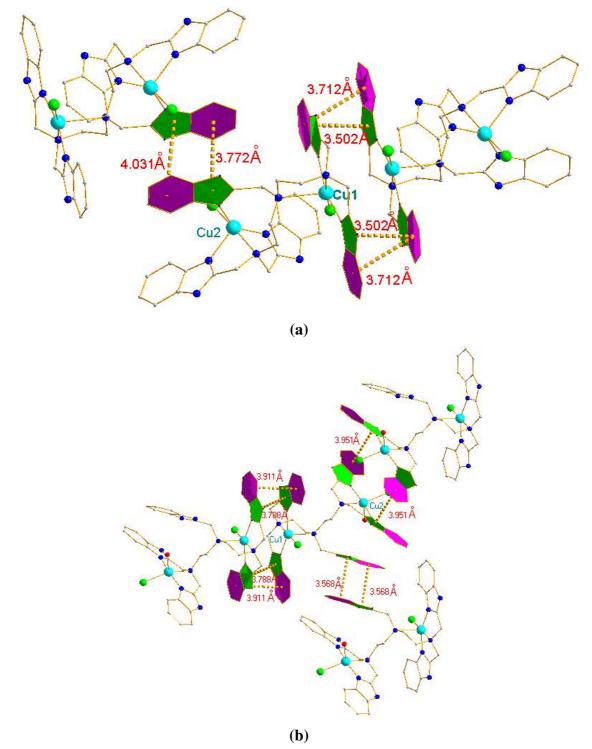


Figure S3. Showing the π - π stacking interactions in 1 (a) and 2 (b). For clarity, solvent molecules, hydrogen atoms and counter anions are omitted. The distances between these symmetry-related centroids are labeled besides the dashed lines.

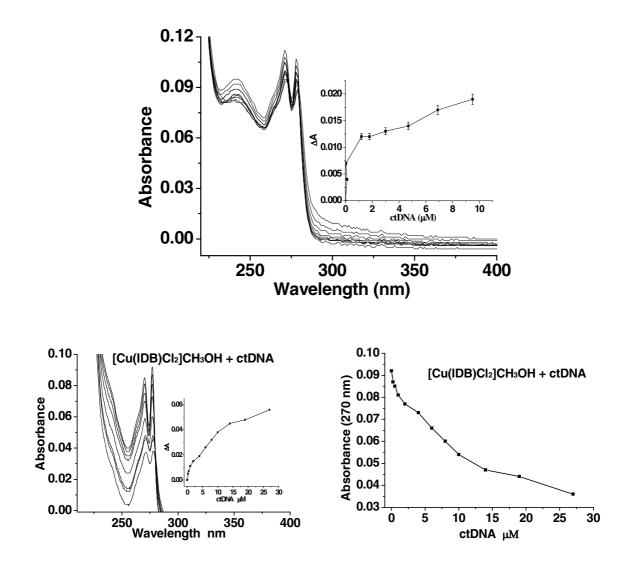


Figure S4. Titration of 1 (4 μ M, upper), 2 (4 μ M, middle) and [Cu(idb)Cl₂]CH₃OH (20 μ M, bottom right and left) with calf thymus DNA (ctDNA, 0–11.10 μ M in base pairs) monitored by UV-visible absorption spectra. The mixtures of 1, 2 or [Cu(idb)Cl₂]CH₃OH with ctDNA were incubated for 3 min at 37 °C in 20 mM Tris-HCl buffer (pH 7.4) prior to measurement. The apparent binding equilibrium constants of each complex to ctDNA were obtained by fitting the changes in absorbance values at 270 nm (Δ A) with the concentration of each complex (inset) to a previously proposed model.⁶

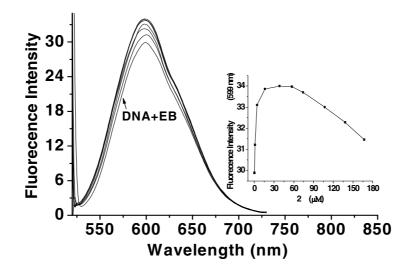


Figure S5. Changes in the fluorescence spectra of (EtBr, excitement wavelength 510 nm) intercalated into ctDNA with concentration of **1**. The complex **1** was increasingly added into the mixture containing ctDNA and EtBr (1:1 for base pair:EtBr) and incubated for 60 s at 37 °C in 20 mM Tris-HCl buffer (pH 7.4) prior to measurement. Addition of **1** (< 45 μ M) leads to DNA condensation and more extensive hydrophobic circumstance around EtBr. Thus, the emission intensity of EtBr was first enhanced (inset). Further addition of **1** (> 45 μ M) causes exclusion of EtBr from the interior of DNA double strands, thereby emission intensity of EtBr being reduced. Here, Δ F is the changes in the fluorescence intensity at 599 nm of EtBr intercalated into ctDNA with concentration of **1**, as shown in the inset.⁷

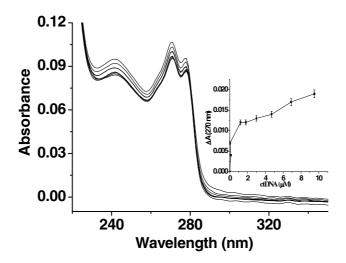


Figure S6. Changes in the absorption spectra of **1** with ctDNA concentration. The mixtures of **1** with ctDNA of increasing concentration were incubated for 60 s at 37 °C in 20 mM Tris-HCl buffer (pH 7.4) prior to measurement. Here, ΔA is the changes in absorbance at 270 nm of **1** with concentration of ctDNA, as shown in the inset.

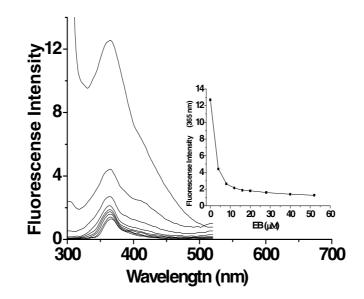


Figure S7. Changes in the fluorescence spectra of **1** (excitement wavelength 270 nm) bound to ctDNA with concentration of EtBr. EtBr was increasingly added into the mixture of ctDNA with **1** (1:1 for base pair: EtBr) and incubated for 60 s at 37 °C in 20 mM Tris-HCl buffer (pH 7.4) prior to measurement. The fluorescence intensity of **1** was progressively reduced upon addition of EtBr. Here, ΔF is the changes in the fluorescence intensity at 365 nm of **1** bound to ctDNA with concentration of EtBr, as shown in the inset.

References:

- (1) Birker, P. J. M. W. L.; Schierbeek, A. J.; Verschoor, G. C.; Reedijk, J. J. Chem. Soc. Chem. Commun. 1981, 1124-1125.
- (2) Adams, H., Bailey, N. A., Carane, J. D. & Fenton, D. E. J. Chem. Soc. Dalton Trans. 1990, 1727–1735.
- (3) Sheldrick, G. M. SHELXS-97: Program for the Solution of Crystal Structure; University of Gottingen: Gottingen, Germany, 1997.
- (4) Sheldrick. G. M. SHELXL-97: Program for the Refinement of Crystal Structure; University of Gottingen: Gottingen, Germany, 1997.
- (5) Spek, A. L. J. Appl. Cryst. 2003, 36, 7--13.
- (6) Wolfe, A.; Shimer, G. H.; Meehan, T. Biochemistry 1987, 26, 6392-6396.
- (7) Sigman, D. S.; Mazuder, A.; Perrin D. M. Chem. Rev. 1993, 93, 2295–2316.